

OIPE

DATE: 02/06/2002 TIME: 11:39:29 RAW SEQUENCE LISTING PATENT APPLICATION: US/09/964,678A

Input Set : A:\seqlist 0609\_4370002 ascii

```
Output Set: N:\CRF3\02062002\1964678A.raw
5 <110> APPLICANT: de la Monte, Suzanne
11 <120> TITLE OF INVENTION: Transgenic Animals and Cell Lines for Screening Drugs
         Effective for the Treatment or Prevention of
         Alzheimer's Disease
12
17 <130> FILE REFERENCE: 0609.4370002
21 <140> CURRENT APPLICATION NUMBER: 09/964,678A
                                                            ENTERED
23 <141> CURRENT FILING DATE: 2001-09-28
27 <150> PRIOR APPLICATION NUMBER: 09/380,203
29 <151> PRIOR FILING DATE: 2000-04-25
 33 <150> PRIOR APPLICATION NUMBER: PCT/US98/03685
 35 <151> PRIOR FILING DATE: 1998-02-26
 39 <150> PRIOR APPLICATION NUMBER: 60/038,908
 41 <151> PRIOR FILING DATE: 1997-02-26
 45 <160> NUMBER OF SEQ ID NOS: 14
 49 <170> SOFTWARE: PatentIn version 3.1
 53 <210> SEQ ID NO: 1
 55 <211> LENGTH: 1442
  57 <212> TYPE: DNA
  59 <213> ORGANISM: Unknown
  63 <220> FEATURE:
  65 <223> OTHER INFORMATION: AD7c-NTP cDNA
  67 <220> FEATURE:
  69 <221> NAME/KEY: CDS
  71 <222> LOCATION: (15)..(1139)
  73 <223> OTHER INFORMATION:
  78 ttttttttt tgag atg gag ttt tcg ctc ttg ttg ccc agg ctg gag tgc
                                                                            50
  77 <400> SEQUENCE: 1
                     Met Glu Phe Ser Leu Leu Leu Pro Arg Leu Glu Cys
                                                                            98
   82 aat ggc gca atc tca gct cac cgc aac ctc cgc ctc ccg ggt tca agc
   79
   83 Asn Gly Ala Ile Ser Ala His Arg Asn Leu Arg Leu Pro Gly Ser Ser
                                                                           146
   86 gat tot cot goo toa goo too coa gta got ggg att aca ggc atg tgc
   87 Asp Ser Pro Ala Ser Ala Ser Pro Val Ala Gly Ile Thr Gly Met Cys
   90 acc cac gct cgg cta att ttg tat ttt ttt tta gta gag atg gag ttt
                                                                            194
   91 Thr His Ala Arg Leu Ile Leu Tyr Phe Phe Leu Val Glu Met Glu Phe
    94 ctc cat gtt ggt cag gct ggt ctc gaa ctc ccg acc tca gat gat ccc
                                                                            242
    95 Leu His Val Gly Gln Ala Gly Leu Glu Leu Pro Thr Ser Asp Asp Pro
    98 tcc gtc tcg gcc tcc caa agt gct aga tac agg act ggc cac cat gcc
                                                                            290
```

RAW SEQUENCE LISTING DATE: 02/06/2002
PATENT APPLICATION: US/09/964,678A TIME: 11:39:29

Input Set : A:\seqlist 0609\_4370002 ascii
Output Set: N:\CRF3\02062002\I964678A.raw

Output Set: N:\CRF3\02002\02002\1300	
99 Ser Val Ser Ala Ser Gln Ser Ala Arg Tyr Arg Thr Gly His His Ala 80 85 90	
on sor Val Ser Ala Ser Gln Ser Ala Arg Tyl Arg 90	338
99 Ser Val Ser Ald Bot 85  100 80  102 cgg ctc tgc ctg gct aat ttt tgt ggt aga aac agg gtt tca ctg atg  102 cgg ctc tgc ctg gct aat ttt tgt ggt aga aac agg gtt tca ctg atg  102 cgg ctc tgc ctg gct aat ttt tgt ggt aga aac agg gtt tca ctg atg	330
100 102 cgg ctc tgc ctg gct aat ttt tgt ggt aga aac agg gct som 102 cgg ctc tgc ctg gct aat ttt tgt ggt aga aac agg gct som 102 cgg ctc tgc ctg gct aat ttt tgt ggt aga aac agg gct som 103 Arg Leu Cys Leu Ala Asn Phe Cys Gly Arg Asn Arg Val Ser Leu Met 105 100 100 100 100 100 100 100 100 100	
102 cgg ccc dy Ala Asn Phe Cys Gly Alg Ash 125	206
103 Arg Leu Cys Leu Ard 100  104  95  106 tgc cca agc tgg tct cct gag ctc aag cag tcc acc tgc ctc agc ctc  106 tgc cca agc tgg tct cct gag ctc aag cag tcc acc tgc ctc agc ctc  107  108  109  109  109  109  109  109  109	386
104 95  106 tgc cca agc tgg tct cct gag ctc aag cag tcc acc tgc ccc agc tgc leu Ser Leu  106 tgc cca agc tgg tct cct gag ctc aag cag tcc acc tgc ccc agc leu Ser Leu  107 Cys Pro Ser Trp Ser Pro Glu Leu Lys Gln Ser Thr Cys Leu Ser Leu  120  115	
106 tgc ccd age sys Ser Pro Glu Leu Lys Gin Sei 111 91	
107 Cys P10 Set 1-1 115 and ggc ctt ttt att	434
107 Cys Pro Ser Trp Ser 115  115  108  110  115  110  110  110 cca aag tgc tgg gat tac agg cgt gca gcc gtg cct ggc ctt ttt att  110 cca aag tgc tgg gat tac agg cgt gca gcc gtg cct ggc ctt ttt att  110 cca aag tgc tgg gat tac agg cgt gca gcc gtg cct ggc ctt ttt att  110 cca aag tgc tgg gat tac agg cgt gca gcc ggc ctt ttt att  111 Pro Lys Cys Trp Asp Tyr Arg Arg Ala Ala Val Pro Gly Leu Phe Ile  111 Pro Lys Cys Trp Asp Tyr Arg Arg Ala Ala Val Pro Gly Leu Phe Ile  1130  130  130  130  135	
110 cca add tye Trp Asp Tyr Arg Arg Ala Ala Val	
111 Pro Lys Cys 117 Asp 17 130 112 125 114 tta ttt tta aga cac agg tgt ccc act ctt acc cag gat gaa gtg 114 tta ttt ttt tta aga cac agg tgt ccc act ctt acc cag gat gaa gtg 114 tta ttt ttt tta aga cac agg tgt ccc act ctt acc cag gat gaa gtg 114 tta ttt ttt tta aga cac agg tgt ccc act ctt acc cag gat gaa gtg 115 The Pho Leu Arg His Arg Cys Pro Thr Leu Thr Gln Asp Glu Val	482
112 125	
112 125  114 tta ttt ttt a aga cac agg tgt ccc act ctt acc cag gdc gd.  114 tta ttt ttt tta aga cac agg tgt ccc act ctt acc cag gdc gd.  115 Leu Phe Phe Leu Arg His Arg Cys Pro Thr Leu Thr Gln Asp Glu Val  115 Leu Phe Phe Leu Arg His Arg Cys Pro Thr Leu Thr Gln Asp Glu Val  155	
115 Leu Phe Phe Leu 145 150	530
116 agg tca ctg cag cct tca act ccc gay	
115 Leu Phe Phe Leu H15  145  116  118 cag tgg tgt gat cac agc tca ctg cag cct tca act cct gag atc aag  118 cag tgg tgt gat cac agc tca ctg cag cct tca act cct gag atc aag  118 cag tgg tgt gat cac agc tca ctg cag cct tra act cct gag atc aag  119 Gln Trp Cys Asp His Ser Ser Leu Gln Pro Ser Thr Pro Glu Ile Lys  119 Gln Trp Cys Asp His Ser Ser Leu Gln Pro Ser Thr Pro Glu Ile Lys  160  165	
119 Gln Trp Cys Asp HIS Ser 3165	578
120 100 100 100 His	
119 Gln Trp Cys Asp Ala Ser Ala Ser Gln Val Ala Gly Thr Lys Asp Met His	
120 160 120 120 120 120 120 120 120 120 120 12	626
124 175 att ttt att ttt aat ttt ttg aga cus	
123 His Pro Pro Ala Ser 180  124  175  180  126 cac tac acc tgg cta att ttt att ttt att ttt aat ttt ttg aga cag  126 cac tac acc tgg cta att ttt att ttt att ttt att ttt aat ttt aga cag  127 The Tro Leu Ile Phe Ile Phe Ile Phe Asn Phe Leu Arg Gln	
	674
128 190 are cag get gga gtg cag tgg cgc aat clt ggc	
127 His Tyr Thr Trp 200  128 190  130 agt ctc aac tct gtc acc cag gct gga gtg cag tgg cgc aat ctt ggc  130 agt ctc aac tct gtc acc cag gct gga gtg cag tgg cgc aat ctt ggc  131 Ser Leu Asn Ser Val Thr Gln Ala Gly Val Gln Trp Arg Asn Leu Gly  210  210  210  210	
131 Ser Leu Asn Ser Val Thr Gin Ald 215	722
131 Ser Leu Ash Ser Val 210  132 205  134 tca ctg caa cct ctg cct ccc ggg ttc aag tta ttc tcc tgc ccc agc  134 tca ctg caa cct ctg cct ccc ggg ttc aag tta ttc tcc tgc ccc agc  235	•
132 205  134 tca ctg caa cct ctg cct ccc ggg ttc aag tta ttc tcc tgg Pro Ser  135 Ser Leu Gln Pro Leu Pro Pro Gly Phe Lys Leu Phe Ser Cys Pro Ser  235  225  230  230  231	
135 Ser Leu Gln Pro Leu Pro Plo Gly 1230	770
136 225	• • •
230  136  225  138 ctc ctg agt agc tgg gac tac agg cgc cca cca cgc cta gct aat ttt  138 ctc ctg agt agc tgg gac tac agg cgc cca cca cgc cta gct aat ttt  138 ctc ctg agt agc tgg gac tac agg cgc cca cca cgc cta gct aat ttt  139 Leu Leu Ser Ser Trp Asp Tyr Arg Arg Pro Pro Arg Leu Ala Asn Phe  250  240  240	
139 Leu Leu Ser Ser Trp Asp Tyl Alg May 245	818
139 Leu Leu Ser Ser 177 245  140 240 245  142 ttt gta ttt tta gta gag atg ggg ttc acc atg ttc gcc agg ttg atc  142 ttt gta ttt tta gta gag atg ggg ttc acc atg ttc gcc agg ttg atc  142 ttt gta ttt tta gta gag atg ggg ttc acc atg ttc gcc agg ttg atc	0
142 ttt gta ttt tta gta gag alg gly Phe Thr Met Phe Ala Arg Leu lie	
140  142 ttt gta ttt tta gta gag atg ggg ttc acc atg tte gee dys  142 ttt gta ttt tta gta gag atg ggg ttc acc atg tte gee dys  143 Phe Val Phe Leu Val Glu Met Gly Phe Thr Met Phe Ala Arg Leu Ile  265  260  265	866
143 Phe Val Phe Hed Val  260  144  255  146 ttg atc tct gga cct tgt gat ctg cct gcc tcg gcc tcc caa agt gct  146 ttg atc tct gga cct tgt gat ctg cct gcc tcg gcc tcc caa agt gct  146 ttg atc tct gga cct tgt gat ctg cct gcc tcg gcc tcc caa agt gct  146 ttg atc tct gga cct tgt gat ctg cct gcc tcg gcc tcc caa agt gct  147 ttg atc tct gga cct tgt gat ctg cct gcc tcg gcc tcc caa agt gct  148 ttg atc tct gga cct tgt gat ctg cct gcc tcg gcc tcc caa agt gct  149 ttg atc tct gga cct tgt gat ctg cct gcc tcg gcc tcc caa agt gct	000
144 255  146 ttg atc tct gga cct tgt gat ctg cct gcc tcg gcc tcc cdd ts 146 ttg atc tct gga cct tgt gat ctg cct gcc tcg gcc tcc cdd ts 147 Leu Ile Ser Gly Pro Cys Asp Leu Pro Ala Ser Ala Ser Gln Ser Ala  147 Leu Ile Ser Gly Pro Cys Asp Leu Pro Ala Ser Ala 280  275 280	
147 Leu Ile Ser Gly Pro Cys Asp Leu Flo Mile 280	914
147 Leu Île Ser GIV 120 275  148 270 275  150 ggg att aca ggc gtg agc cac cac gcc cgg ctt att ttt aat ttt tgt  150 ggg att aca ggc gtg agc cac cac gcc cgg ctt att ttt aat ttt tgt  150 ggg att aca ggc gtg agc cac cac gcc cgg ctt att ttt aat ttt tgt  150 ggg att aca ggc gtg agc cac cac gcc cgg ctt att ttt aat ttt tgt  150 ggg att aca ggc gtg agc cac cac gcc cgg ctt att ttt aat ttt tgt  150 ggg att aca ggc gtg agc cac cac gcc cgg ctt att ttt aat ttt tgt  150 ggg att aca ggc gtg agc cac cac gcc cgg ctt att ttt aat ttt tgt	714
148 270  150 ggg att aca ggc gtg agc cac cac gcc cgg ctt att tit dat de sol 150 ggg att aca ggc gtg agc cac cac gcc cgg ctt att tit dat de sol 150 ggg att aca ggc gtg agc cac cac gcc cgg ctt att tit dat de sol 150 ggg att aca ggc ggg gtg cac cac gcc cgg ctt att tit dat de sol 150 ggg gtg cac cac gcc cgg ctt att tit dat de sol 150 ggg gtg cac cac gcc cgg ctt att tit dat de sol 150 ggg gtg cac cac cac gcc cgg ctt att tit dat de sol 150 ggg gtg cac cac cac gcc cgg ctt att tit dat de sol 150 ggg gtg cac cac cac gcc cgg ctt att tit dat de sol 150 ggg gtg cac cac cac gcc cgg ctt att tit dat de sol 150 ggg gtg cac cac cac gcc cgg ctt att tit dat de sol 150 ggg gtg cac cac cac gcc cgg ctt att tit dat de sol 150 ggg gtg cac cac cac gcc cgg ctt att tit dat de sol 150 ggg gtg cac cac cac gcc cgg ctt att tit dat de sol 150 ggg gtg cac cac cac gcc cgg ctt att tit dat de sol 150 ggg gtg cac cac cac gcc cgg ctt att tit dat de sol 150 ggg gtg cac cac cac gcc cgg ctt att tit dat de sol 150 ggg gtg cac cac cac gcc cgg ctt att tit dat de sol 150 ggg gtg cac cac cac gcc cgg ctt att tit dat de sol 150 ggg gtg cac cac cac gcc cgg ctt att tit dat de sol 150 ggg gtg cac cac cac gcc cgg ctt att tit dat de sol 150 ggg gtg cac cac cac gcc cgg ctt att tit dat de sol 150 ggg gtg gtg cac cac cac gcc cgg ctt att tit dat de sol 150 ggg gtg gtg gtg cac cac cac gcc cgg ctt att tit dat de sol 150 ggg gtg gtg gtg gtg gtg gtg gtg gtg gt	
150 ggg are Thr Gly Val Ser His HIS Ala Alg 295	962
151 Gly Ile Thr Gly Val 290  152 285  154 ttg ttt gaa atg gaa tct cac tct gtt acc cag gct gga gtg caa tgg  154 ttg ttt gaa atg gaa tct cac tct gtt acc cag gct gga gtg caa tgg  154 ttg ttt gaa atg gaa tct cac tct gtt acc cag gct gga gtg caa tgg  154 ttg ttt gaa atg gaa tct cac tct gtt acc cag gct gga gtg caa tgg  154 ttg ttt gaa atg gaa tct cac tct gtt acc cag gct gga gtg caa tgg  154 ttg ttt gaa atg gaa tct cac tct gtt acc cag gct gga gtg caa tgg  155 The column of the colu	902
152 203	
152 285 154 ttg ttt gaa atg gaa tct cac tct gtt acc cag gct gga gcs 154 ttg ttt gaa atg gaa tct cac tct gtt acc cag gct gga gcs 155 Leu Phe Glu Met Glu Ser His Ser Val Thr Gln Ala Gly Val Gln Trp 155 Leu Phe Glu Met Glu Ser His Ser Val Thr Gln Ala Gly Val Gln Trp 155 Leu Phe Glu Met Glu Ser His Ser Val Thr Gln Ala Gly Val Gln Trp 155 Leu Phe Glu Met Glu Ser His Ser Val Thr Gln Ala Gly Val Gln Trp 156 Leu Phe Glu Met Glu Ser His Ser Val Thr Gln Ala Gly Val Gln Trp 157 Leu Phe Glu Met Glu Ser His Ser Val Thr Gln Ala Gly Val Gln Trp 158 Leu Phe Glu Met Glu Ser His Ser Val Thr Gln Ala Gly Val Gln Trp 159 Leu Phe Glu Met Glu Ser His Ser Val Thr Gln Ala Gly Val Gln Trp 150 Leu Phe Glu Met Glu Ser His Ser Val Thr Gln Ala Gly Val Gln Trp	1010
305 and and oth and the state of the state o	1010
155 Leu Phe Glu Met 315 310  156 305 305  158 cca aat ctc ggc tca ctg caa cct ctg cct ccc ggg ctc aag cga ttc  158 cca aat ctc ggc tca ctg caa cct ctg pro Pro Gly Leu Lys Arg Phe  159 Pro Asn Leu Gly Ser Leu Gln Pro Leu Pro Pro Gly Leu Lys Arg Phe  330  320	
158 CCa dat CCo SJ. Ser Leu Gln Pro Leu Pro Pro Sil 2330	1050
159 Pro Ash Box 320 325	1058
159 Pro Ash Leu GI7  320  160  162 tcc tgt ctc agc ctc cca agc agc tgg gat tac ggg cac ctg cca cca  162 tcc tgt ctc agc ctc cca agc agc tgg gat tac ggg cac ctg cca cca  162 tcc tgt ctc agc ctc cca agc agc tgg gat tac ggg cac ctg cca cca  162 tcc tgt ctc agc ctc cca agc agc tgg gat tac ggg cac ctg cca cca	
160  162 tcc tgt ctc agc ctc cca agc agc tgg gat tac ggg cdc orgin 162 tcc tgt ctc agc ctc cca agc agc tgg gat tac ggg cdc orgin 162 tcc tgt ctc agc ctc cca agc agc tgg gat tac ggg cdc orgin 162 tcc tgt ctc agc ctc cca agc agc tgg gat tac ggg cdc orgin 162 tcc tgt ctc agc ctc cca agc agc tgg gat tac ggg cdc orgin 162 tcc tgt ctc agc ctc cca agc agc tgg gat tac ggg cdc orgin 162 tcc tgt ctc agc ctc cca agc agc tgg gat tac ggg cdc orgin 162 tcc tgt ctc agc ctc cca agc agc tgg gat tac ggg cdc orgin 162 tcc tgt ctc agc ctc cca agc agc tgg gat tac ggg cdc orgin 162 tcc tgt ctc agc ctc cca agc agc tgg gat tac ggg cdc orgin 162 tcc tgt ctc agc ctc cca agc agc tgg gat tac ggg cdc orgin 162 tcc tgt ctc agc ctc cca agc agc tgg gat tac ggg cdc orgin 162 tcc tgt ctc agc ctc cca agc agc tgg gat tac ggg cdc orgin 162 tcc tgt ctc agc ctc cca agc agc tgg gat tac ggg cdc orgin 162 tcc tgt ctc agc ctc cca agc agc tgg gat tac ggg cdc orgin 162 tcc tgt ctc agc ctc cca agc agc agc tgg gat tac ggg cdc orgin 162 tcc tgt ctc agc agc agc agc agc agc agc agc agc ag	
103 Set Cla non -	

DATE: 02/06/2002 TIME: 11:39:29 RAW SEQUENCE LISTING PATENT APPLICATION: US/09/964,678A

Input Set : A:\seqlist 0609\_4370002 ascii
Output Set: N:\CRF3\02062002\I964678A.raw

Output Set: N:\CRF3\02062002\1964076115	
Output Sec. 2.0 (	1106
340 cca tat	1106
335 at the att aga ggc ggg gtt car Pro Tyr	
164 at the tight at the Arg Gly Gly Val Ser 125 pho Tle Arg Gly Gly Gly Val Ser 125 pho Tle Arg Gly Gly Gly Val Ser 125 pho Tle Arg Gly	
164 335 340 345  166 cac ccc gct aat ttt tgt att ttc att aga ggc ggg gtt tca cca tat  167 His Pro Ala Asn Phe Cys Ile Phe Ile Arg Gly Gly Val Ser Pro Tyr  168 350 355  170 ttg tca ggc tgg tct caa act cct gac ctc agg tgacccacct gcctcagcct  170 ttg tca ggc tgg tct caa act cct gac ctc agg tgacccacct gcctcagcct  170 trg tca ggc tgg tct caa act cct gac ctc agg tgacccacct gcctcagacct  170 trg tca ggc tgg tct caa act cct gac ctc agg tgacccacct gcctcagacct	1159
167 His PIO Ale 355	
168 350 reg tag tet caa act cet gas tou Arg	
168 350 170 ttg tca ggc tgg tct caa act cct gdc Arg 170 ttg tca ggc tgg tct caa act cct gdc Arg 171 Leu Ser Gly Trp Ser Gln Thr Pro Asp Leu Arg 171 Leu Ser Gly Trp Ser Gln Thr Pro Asp Leu Arg 170 375 375 375 375 375 375 375 375 375 375	1219
	1279
	1339
170 ttg tod 375  171 Leu Ser Gly Trp Ser Gln Thr P10 the 375  172 365  174 tecaaagtge tgggattaca ggegtgagee aceteaceca geeggetaat ttagataaaa ettetggett  174 tecaaagtge tgggattaca ggegtgatat ttgcccagge tggteteaaa ettetggett  175 realtatgtag caatgggggg tettgetatg ttgcccagge acattttta aacagttaca	
171 Lett 3c1 370 172 365 174 tccaaagtgc tgggattaca ggcgtgagcc acctcaccca gccggctaat ttagton 174 tccaaagtgc tgggattaca ggcgtgagcc ttgcccaggc tggtctcaaa cttctggctt 176 aaatatgtag caatgggggg tcttgctatg ttgcccaggc acattttta aacagttaca 178 catgcaatcc ttccaaatga gccacaacac ccagccagtc acattttta aacagttaca 178 catgcaatcc ttccaaatga aaagtaatac aataaacatg tcaaacctgc aaattcagta	1399
170 Catgcaatcc ttccaaatga gccaataatac aataaacatg tcaaacctg	1442
174 tecandagos caatgggggg tettgetaty 55 176 aaatatgtag caatgggggg tettgetaty 55 178 catgcaatcc ttecaaatga gecacaacac ceagecagte acattttta adeays 178 catgcaatcc ttecaaatga gecacaacac aataaacatg teaaaectge aaatteagta 180 tetttattt agtatactag aaagtaatac aataaacatg gea 182 gtaacagagt tettttataa ettttaaaca aagetttaga gea 182 gtaacagagt tettttataa ettttaaaca aagetttaga gea	
182 gtaacagus 185 <210> SEQ ID NO: 2	
185 <210	
187 (212) TYPE: PRT 189 (212) TYPE: PRT  ORGANISM: Unknown	
189 <212> TYPE: TAX- 191 <213> ORGANISM: Unknown	
10E /220> FEATURE: 3D70-NTP CDNA	
191 <220> FEATURE: 195 <220> FEATURE: 197 <223> OTHER INFORMATION: AD7c-NTP cDNA 197 <203> OTHER INFORMATION: AD7c-NTP cDNA 199 <400> SEQUENCE: 2 199 <400> SEQUENCE: 2 10 10 10 10 10 10 10 10 10 10 10 10 10	
TOO MADO SHOULDINGS.	
201 Met Glu Phe Ser Leu Leu Leu Pro Horizon 10 202 1 205 Ser Ala His Arg Asn Leu Arg Leu Pro Gly Ser Ser Asp Ser Pro Ala 205 Ser Ala His Arg Asn Leu Arg Leu Pro Gly Met Cys Thr His Ala Arg 20 The Thr Gly Met Cys Thr His Ala Arg	
205 Ser Ala His Arg Ash Leu Arg 25	
205 Ser Ala His Arg Asn Leu Arg Bet 25 206 20 20 25 207 45 208 Ser Ala Ser Pro Val Ala Gly Ile Thr Gly Met Cys Thr His Ala Arg 209 Ser Ala Ser Pro Val Ala Gly Het Glu Phe Leu His Val Gly 309 Yel Clu Met Glu Phe Leu His Val Gly	
200 Ser Ala Ser Pro Val Ala Gly 11c 145 209 Ser Ala Ser Pro Val Ala Gly 11c 145 210 35 211 Leu Ile Leu Tyr Phe Phe Leu Val Glu Met Glu Phe Leu His Val Gly 213 Leu Ile Leu Tyr Phe Phe Leu Val Glu Met Glu Phe Leu His Val Gly 60 213 Leu Ile Leu Tyr Phe Phe Ser Asp Asp Pro Ser Val Ser Ala	
210 60 cm le Leu Tyr Phe Phe Leu Val Car Ala	
213 Leu Ile Leu Tyr Phe Phe Leu Vul 60 213 Leu Ile Leu Tyr Phe Phe Leu Vul 60 214 50 214 50 217 Gln Ala Gly Leu Glu Leu Pro Thr Ser Asp Asp Pro Ser Val Ser Ala 75 70 71 Cly His His Ala Arg Leu Cys Leu	
217 Gin Ala Gir 70 70 Ris His Ala Arg Leu Cys	
240 6b 3-4 WAT GIV 11-4 W	
214 217 Gln Ala Gly Leu Glu Leu Pro III	
225 Ala Asn Phe Cys Gir 105 105 Car Leu Pro Lys Cys Trp	
225 Ala Asn Phe Cys Gly Arg Ash Arg 105 226 100 229 Ser Pro Glu Leu Lys Gln Ser Thr Cys Leu Pro Lys Cys Trp 120 121 125 126 127 128 128 129 120 120 120 120 120 120 120 120 120 120	
233 Asp Tyr Arg Arg Ala Ala Val Plo 327  234 130  237 Arg His Arg Cys Pro Thr Leu Thr Gln Asp Glu Val Gln Trp Cys Asp  155  150  175	)
254 Arg His Arg Cys Pro Thr Let 115 155 Pro Pro Ale	ì
234 237 Arg His Arg Cys Pro Thr Leu III 255 155 238 145 241 His Ser Ser Leu Gln Pro Ser Thr Pro Glu Ile Lys His Pro Pro Ala 175 170 165 241 His Ser Ser Leu Gln Pro Ser Thr Lys Asp Met His His Tyr Thr Tr	
238 143 Ser Ser Leu Gln Pro Ser IIII 170	0
241 His Set 165 The Lys Asp Met His His Tyr Int 121	•
242 Ala Ser Gln Val Ala Gly Thi Lys 195	r
241 His Ser Ser Leu Gln Pro Ser The 170 242 245 Ser Ala Ser Gln Val Ala Gly Thr Lys Asp Met His His Tyr Thr Try 246 246 249 Leu Ile Phe Ile Phe Ile Phe Asn Phe Leu Arg Gln Ser Leu Asn Se 200 200 200 200 201 202 203 204 205 207 207 208 209 209 200 200 200 200 200 200 200 200	-
0.4.6 - DEO AGN PHO DOW - 0.0.6	
249 Leu Ile Phe Ile Phe Ile Phe 200 250 250 250 250 253 Val Thr Gln Ala Gly Val Gln Trp Arg Asn Leu Gly Ser Leu Gln Pr 250 250 250 250 250 250 250 260 270 270 270 270 270 270 270 270 270 27	U
250 253 Val Thr Gln Ala Gly Val Gli 11p 125 254 215 254 210 257 Leu Pro Pro Gly Phe Lys Leu Phe Ser Cys Pro Ser Leu Leu Ser Se 235 230	5T
254 210 Phe Lys Leu Phe Ser Cys P10 335	10
257 Leu Pro Pro Gry 1230	
258 225	

DATE: 02/06/2002 TIME: 11:39:29 RAW SEQUENCE LISTING PATENT APPLICATION: US/09/964,678A

Input Set : A:\seqlist 0609\_4370002 ascii

Output Set: N:\CRF3\02062002\1964678A.raw

```
261 Trp Asp Tyr Arg Arg Pro Pro Arg Leu Ala Asn Phe Phe Val Phe Leu
265 Val Glu Met Gly Phe Thr Met Phe Ala Arg Leu Ile Leu Ile Ser Gly
269 Pro Cys Asp Leu Pro Ala Ser Ala Ser Gln Ser Ala Gly Ile Thr Gly
273 Val Ser His His Ala Arg Leu Ile Phe Asn Phe Cys Leu Phe Glu Met
277 Glu Ser His Ser Val Thr Gln Ala Gly Val Gln Trp Pro Asn Leu Gly
 281 Ser Leu Gln Pro Leu Pro Pro Gly Leu Lys Arg Phe Ser Cys Leu Ser
 285 Leu Pro Ser Ser Trp Asp Tyr Gly His Leu Pro Pro His Pro Ala Asn
 289 Phe Cys Ile Phe Ile Arg Gly Gly Val Ser Pro Tyr Leu Ser Gly Trp
             355
 290
 293 Ser Gln Thr Pro Asp Leu Arg
          370
  294
  297 <210> SEQ ID NO: 3
  299 <211> LENGTH: 1381
  301 <212> TYPE: DNA
  303 <213> ORGANISM: Unknown
  309 <223> OTHER INFORMATION: Incorrect sequence of AD7c-NTP DNA
  307 <220> FEATURE:
  312 tttttttt gagatggagt tttcgctctt gttgcccagg ctggagtgca atggcgcaat
                                                                              60
  314 ctcagctcac egcaacetee gecteeeggg ttcaagegat teteetgeet cageeteeee
                                                                             120
   316 agtagctggg attacaggca tgtgcaccac gctcggctaa ttttgtattt ttttttagta
                                                                             180
   318 gagatggagt ttaactccat gttggtcagg ctggtctcga actcccgacc tcagatgatc
                                                                             240
   320 tecegteteg geetgeecaa agtgetgaga ttacaggeat gagecaccat geeeggeete
                                                                             300
   322 tgcctggcta atttttgtgg tagaaacagg gtttcactga tgttgcccaa gctggtctcc
                                                                             360
   324 tgagetcaag cagtecacet geetcageet eccaaagtge tgggattaca ggegteagee
                                                                             420
   326 gtgcctggcc tttttatttt attttttta agacacaggt gtaccactct tacccaggat
                                                                             480
   328 gaagtgcagt ggtgtgatca cagetcactg cageettcaa eteetgagat caageaatee
                                                                             540
   330 tectgeetea geeteccaag tagetgggae caaagacatg caccactaca eetggtaatt
                                                                              600
   332 tttatttta tttttaattt tttgagacag agtctcactc tgtcacccag gctggagtgc
                                                                              660
   334 agtggcgcaa tcttggctca ctgcaacctc tgcctcccgg gttcaagtta ttctcctgcc
                                                                              720
    336 ccagcetect gagtagetgg gactacagge geccaceaeg ectagetaat ttttttgtat
                                                                              780
    338 ttttagtaga gatggggttt caccatgttc gccaggttga tcttgatctc ttgaccttgt
                                                                              840
    340 gatctgcctg cctcggccta cccaaagtgc tgggattaca ggtcgtgact ccacgccggc
                                                                              900
    342 ctatttttaa tttttgtttg tttgaaatgg aatctcactc tgttacccag gtcggagtgc
                                                                              960
    344 aatggcaaat ctcggctact cgcaacctet gcctcccggg tcaagcgatt ctcctgtetc
                                                                             1020
    346 agoctoccaa goagotggga ttacgggaco tgcaccacao cocgotaatt tttgtattt
                                                                             1080
    348 cattagagge gggtttacca tatttgtcag getgggtete aaacteetga eetcaggtga
                                                                             1140
    350 cccacctgcc tcagcettcc aaagtgctgg gattacaggc gtgagccacc tcacccagec
                                                                              1200
    352 ggctaatttg gaataaaaaa tatgtagcaa tgggggtctg ctatgttgcc caggctggtc
                                                                              1260
    354 toaaacttot ggottoagto aatoottoca aatgagocao aacaccoago cagtoacatt
                                                                              1320
     356 ttttaaacag ttacatcttt attttagtat actagaaagt aatacaataa acatgtcaaa
                                                                              1380
                                                                              1381
     358 C
```

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/964,678A

DATE: 02/06/2002 TIME: 11:39:29

Input Set : A:\seqlist 0609\_4370002 ascii Output Set: N:\CRF3\02062002\1964678A.raw

361 <210> SEQ ID NO: 4 363 <211> LENGTH: 1418 365 <212> TYPE: DNA 367 <213> ORGANISM: Unknown 373 <223> OTHER INFORMATION: Incorrect sequence of AD7c-NTP cDNA 376 ttttttttt gagatggagt tttcgctctt gttgcccagg ctggagtgca atggcgcaat 60 375 <400> SEQUENCE: 4 378 ctcagetcac egcaacetee geeteeeggg ttcaagegat teteetgeet cageeteeee 120 380 agtaggctgg gattacaggc atgtgcacca cgctcggcta attttgtatt ttttttagt 180 382 agagatggag tttctccatg ttggtcaggc tggtctcgaa ctccgacctc agatgatcct 240 384 cccgtctcgg cctcccaaag tgctagatac aggactgagc accatgcccg gcctctgcct 300 386 ggctaattit tgtggtagaa acagggttte actgatgtge ceaagetggt eteetgaget 360 388 caagcagtcc acctgcctca gcctcccaaa gtgctgggat tacaggcgtg cagccgtgcc 420 390 tggccttttt attttatttt ttttaagaca caggtgtccc actcttaccc aggatgaagt 480 392 gcagtggtgt gatcacaget cactgcagec ttcaactetg agatcaagea tecteetgee 540 394 tcagcctccc aaagtagctg ggaccaaaga catgcaccac tacacctggc taattttat 600 396 ttttatttt aatttttga gacagagtet caactetgte acceaggetg gagtgeagtg 660 398 gcgcaatctt ggctcactgc aacctctgcc tcccgggttc aagttattct cctgccccag 720 400 cctcctgagt agctgggact acaggcgccc accacgccta gctaatttt ttgtatttt 780 402 agtagagatg gggtttcacc atgttcgcca ggttgatgct agatetettg accttgtgat 840 404 ctgcctgcct cggcctccca aagtgctggg attacaggac gtgacgccca ccgcccggcc 900 406 tatttttaat ttttgtttgt ttgaaatgga atctcactct gttacccagg ctggagtgca 960 408 atggccaaat ctcggctcac tgcaacctct gcctcccggg ctcaagcgat tctcctgtct 1020 410 cagcetecca ageagetggg attacgggea cetgeaceae acceegetaa tttttgtatt 1080 412 ttcattagag gcggggtttc accatatttg tcaggctggt ctcaaactcc tgacctcagg 1140 414 tgacccacct gcctcagcct tccaaagtgc tgggattaca ggcgtgacgc ctcacccagc 1200 416 cggctaattt agataaaaaa atatgtagca atggggggtc ttgctatgtt gcccaggctg 1260 418 gtctcaaact tctggcttca tgcaatcctt ccaaatgagc cacaacaccc agccagtcac 1320 420 atttttaaac agttacatct ttattttagt atactagaaa gtgatacgat aacatggcgg 1380 1418 422 aacctgcaaa ttcgagtagt acagagtctt ttataact 425 <210> SEQ ID NO: 5 427 <211> LENGTH: 22 429 <212> TYPE: DNA 431 <213> ORGANISM: Artificial Sequence 437 <223> OTHER INFORMATION: AD7c-NTP oligonucleotide 22 439 <400> SEQUENCE: 5 440 tgtcccactc ttacccagga tg 443 <210> SEQ ID NO: 6 445 <211> LENGTH: 24 447 <212> TYPE: DNA 449 <213> ORGANISM: Artificial Sequence 455 <223> OTHER INFORMATION: AD7c-NTP oligonucleotide 457 <400> SEQUENCE: 6 458 aagcaggcag atcacaaggt ccag 461 <210> SEQ ID NO: 7

Use of n and/or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.

463 <211> LENGTH: 20

24

VERIFICATION SUMMARY

DATE: 02/06/2002

PATENT APPLICATION: US/09/964,678A

TIME: 11:39:30

Input Set : A:\seqlist 0609\_4370002 ascii Output Set: N:\CRF3\02062002\1964678A.raw

L:576 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 L:604 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 L:632 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14